

SEQUENCE LISTING

<110> MIYATA, Toshio
KUROKAWA, Kiyoshi

<120> Megsin Protein

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<150> JP09-275302

<151> 1997-09-22

<160> 44

<170> PatentIn Ver. 2.0

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<211> 1143

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(1140)

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aga gag atg gat gac aat caa gga aat gga aat gtg ttc ttt tcc tct	96
Arg Glu Met Asp Asp Asn Gln Gly Asn Gly Asn Val Phe Phe Ser Ser	
20 25 30	
ctg agc ctc ttc gct gcc ctg gcc ctg gtc cgc ttg ggc gct caa gat	144
Leu Ser Leu Phe Ala Ala Leu Ala Leu Val Arg Leu Gly Ala Gln Asp	
35 40 45	
gac tcc ctc tct cag att gat aag ttg ctt cat gtt aac act gcc tca	192
Asp Ser Leu Ser Gln Ile Asp Lys Leu Leu His Val Asn Thr Ala Ser	
50 55 60	
gga tat gga aac tct tct aat agt cag tca ggg ctc cag tct caa ctg	240
Gly Tyr Gly Asn Ser Ser Asn Ser Gln Ser Gly Leu Gln Ser Gln Leu	
65 70 75 80	
aaa aga gtt ttt tct gat ata aat gca tcc cac aag gat tat gat ctc	288
Lys Arg Val Phe Ser Asp Ile Asn Ala Ser His Lys Asp Tyr Asp Leu	
85 90 95	
agc att gtg aat ggg ctt ttt gct gaa aaa gtg tat ggc ttt cat aag	336
Ser Ile Val Asn Gly Leu Phe Ala Glu Lys Val Tyr Gly Phe His Lys	
100 105 110	
gac tac att gag tgt gcc gaa aaa tta tac gat gcc aaa gtg gag cga	384
Asp Tyr Ile Glu Cys Ala Glu Lys Leu Tyr Asp Ala Lys Val Glu Arg	
115 120 125	

gtt gac ttt acg aat cat tta gaa gac act aga cgt aat att aat aag Val Asp Phe Thr Asn His Leu Glu Asp Thr Arg Arg Asn Ile Asn Lys 130 135 140	432
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aat cta atg gaa tgg acc aat cca agg cga atg acc tct aag tat gtt Asn Leu Met Glu Trp Thr Asn Pro Arg Arg Met Thr Ser Lys Tyr Val 260 265 270	816
gag gta ttt ttt cct cag ttc aag ata gag aag aat tat gaa atg aaa Glu Val Phe Phe Pro Gln Phe Lys Ile Glu Lys Asn Tyr Tyr Met Lys 275 280 285	864
caa tat ttg aga gcc cta ggg ctg aaa gat atc ttt gat gaa tcc aaa Gln Tyr Leu Arg Ala Leu Gly Leu Lys Asp Ile Phe Asp Glu Ser Lys 290 295 300	912
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atg atg cac aaa tct tac ata gag gtc act gag gag ggc acc gag gct Met Met His Lys Ser Tyr Ile Glu Val Thr Glu Glu Gly Thr Glu Ala 325 330 335	1008
act gct gcc aca gga agt aat att gta gaa aag caa ctg cct cag tcc Thr Ala Ala Thr Gly Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser 340 345 350	1056
acg ctg ttt aga gct gac cac cca ttc cta ttt gtt atc agg aag gat Thr Leu Phe Arg Ala Asp His Pro Phe Leu Phe Val Ile Arg Lys Asp 355 360 365	1104

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1143

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 35 40 45
 Asp Ser Leu Ser Gln Ile Asp Lys Leu Leu His Val Asn Thr Ala Ser
 50 55 60
 Gly Tyr Gly Asn Ser Ser Asn Ser Gln Ser Gly Leu Gln Ser Gln Leu
 65 70 75 80
 Lys Arg Val Phe Ser Asp Ile Asn Ala Ser His Lys Asp Tyr Asp Leu
 85 90 95
 Ser Ile Val Asn Gly Leu Phe Ala Glu Lys Val Tyr Gly Phe His Lys
 100 105 110
 Asp Tyr Ile Glu Cys Ala Glu Lys Leu Tyr Asp Ala Lys Val Glu Arg
 115 120 125
 Val Asp Phe Thr Asn His Leu Glu Asp Thr Arg Arg Asn Ile Asn Lys
 130 135 140
 Trp Val Glu Asn Glu Thr His Gly Lys Ile Lys Asn Val Ile Gly Glu
 145 150 155 160
 Gly Gly Ile Ser Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr
 165 170 175
 Phe Lys Gly Lys Trp Gln Ser Ala Phe Thr Lys Ser Glu Thr Ile Asn
 180 185 190
 Cys His Phe Lys Ser Pro Lys Cys Ser Gly Lys Ala Val Ala Met Met
 195 200 205
 His Gln Glu Arg Lys Phe Asn Leu Ser Val Ile Glu Asp Pro Ser Met
 210 215 220
 Lys Ile Leu Glu Leu Arg Tyr Asn Gly Gly Ile Asn Met Tyr Val Leu
 225 230 235 240
 Leu Pro Glu Asn Asp Leu Ser Glu Ile Glu Asn Lys Leu Thr Phe Gln
 245 250 255

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Asn Leu Met Glu Trp Thr Asn Pro Arg Arg Met Thr Ser Lys Tyr Val
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Glu Val Phe Phe Pro Gln Phe Lys Ile Glu Lys Asn Tyr Glu Met Lys
    275                      280                      285
Gln Tyr Leu Arg Ala Leu Gly Leu Lys Asp Ile Phe Asp Glu Ser Lys
    290                      295                      300
Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Ile Ser Arg
    305                      310                      315                      320
Met Met His Lys Ser Tyr Ile Glu Val Thr Glu Glu Gly Thr Glu Ala
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Thr Ala Ala Thr Gly Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser
    340                      345                      350
Thr Leu Phe Arg Ala Asp His Pro Phe Leu Phe Val Ile Arg Lys Asp
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Asp Ile Ile Leu Phe Ser Gly Lys Val Ser Cys Pro
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<222> (8)..(1147)

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Leu Phe Arg Glu Met Asp Ser Ser Gln Gly Asn Gly Asn Val Phe Phe
  15                      20                      25                      30

tct tcc ctg agc atc ttc act gcc ctg agc cta atc cgt ttg ggt gct 145
Ser Ser Leu Ser Ile Phe Thr Ala Leu Ser Leu Ile Arg Leu Gly Ala
        35                      40                      45

cga ggt gac tgt nnn cgt cag att gac aag gcc ctg cac ttt atc tcc 193
Arg Gly Asp Cys Xaa Arg Gln Ile Asp Lys Ala Leu His Phe Ile Ser
        50                      55                      60

cca tca aga caa ggg aat tca tcg aac agt cag cta gga ctg caa tat 241
Pro Ser Arg Gln Gly Asn Ser Ser Asn Ser Gln Leu Gly Leu Gln Tyr
        65                      70                      75

caa ttg aaa aga gtt ctt gct gac ata aac tca tct cat aag gat nnn 289
Gln Leu Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys Asp Xaa
  80                      85                      90

aaa ctc agc att gcc aat gga gtt ttt gca gag aaa gta ttt gat ttt 337

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Lys 95	Leu	Ser	Ile	Ala	Asn 100	Gly	Val	Phe	Ala	Glu 105	Lys	Val	Phe	Asp	Phe 110	
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His	Lys	Ser	Tyr	Met 115	Glu	Cys	Ala	Glu	Asn 120	Leu	Tyr	Asn	Ala	Lys 125	Val	
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Glu	Arg	Val	Asp 130	Phe	Thr	Asn	Asp	Ile 135	Gln	Glu	Thr	Arg	Phe 140	Lys	Ile	
aat	aaa	tgg	att	gaa	aat	gaa	aca	cat	ggc	aaa	atc	aag	aag	gtg	ttg	481
Asn	Lys	Trp 145	Ile	Glu	Asn	Glu	Thr 150	His	Gly	Lys	Ile	Lys 155	Lys	Val	Leu	
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Pro	Met	Gln 225	Ile	Leu	Glu	Leu	Gln 230	Tyr	His	Gly	Gly	Ile 235	Ser	Met	Tyr	
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Ser	Lys	Leu 320	Met	His	Lys	Ser 325	Leu	Ile	Glu	Val	Ser 330	Glu	Glu	Gly	Thr	
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Glu Ala Thr Ala Ala Thr Glu Ser Asn Ile Val Glu Lys Leu Leu Pro
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 355 360 365
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 Asp Cys Xaa Arg Gln Ile Asp Lys Ala Leu His Phe Ile Ser Pro Ser
 50 55 60
 Arg Gln Gly Asn Ser Ser Asn Ser Gln Leu Gly Leu Gln Tyr Gln Leu
 65 70 75 80
 Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys Asp Xaa Lys Leu
 85 90 95
 Ser Ile Ala Asn Gly Val Phe Ala Glu Lys Val Phe Asp Phe His Lys
 100 105 110
 Ser Tyr Met Glu Cys Ala Glu Asn Leu Tyr Asn Ala Lys Val Glu Arg
 115 120 125
 Val Asp Phe Thr Asn Asp Ile Gln Glu Thr Arg Phe Lys Ile Asn Lys
 130 135 140
 Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys Val Leu Gly Asp
 145 150 155 160
 Ser Ser Leu Ser Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr
 165 170 175
 Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Ser Asp Thr Leu Ser
 180 185 190
 Cys His Phe Arg Ser Pro Ser Gly Pro Gly Lys Ala Val Asn Met Met
 195 200 205

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His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln Glu Pro Pro Met
 210                215                220

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Leu Pro Glu Asp Asp Leu Ser Glu Ile Glu Ser Lys Leu Ser Phe Gln
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Asn Leu Met Asp Trp Thr Asn Ser Arg Lys Met Lys Ser Gln Tyr Val
                260                265                270

Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asp Tyr Glu Met Arg
 275                280                285

Ser His Leu Lys Ser Val Gly Leu Glu Asp Ile Phe Val Glu Ser Arg
 290                295                300

Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Val Ser Lys
 305                310                315                320

Leu Met His Lys Ser Leu Ile Glu Val Ser Glu Glu Gly Thr Glu Ala
                325                330                335

Thr Ala Ala Thr Glu Ser Asn Ile Val Glu Lys Leu Leu Pro Glu Ser
                340                345                350

Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val Ile Arg Lys Asn
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Gly Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro
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<213> Mus musculus

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ttc ttc tct tcc ctg agc atc ttc act gcc ctg acc cta atc cgt ctg      96
Phe Phe Ser Ser Leu Ser Ile Phe Thr Ala Leu Thr Leu Ile Arg Leu
                20                25                30

ggt gct cga ggt gac tgt gca cgt cag att gac aag gca ctg cac ttt      144
Gly Ala Arg Gly Asp Cys Ala Arg Gln Ile Asp Lys Ala Leu His Phe
                35                40                45

aac ata cca tca aga caa gga aac tca tct aat aat cag cca gga ctt      192
Asn Ile Pro Ser Arg Gln Gly Asn Ser Ser Asn Asn Gln Pro Gly Leu
 50                55                60

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gat tat gaa ctc agc att gcc act gga gtt ttt gca gaa aaa gtc tat	288
Asp Tyr Glu Leu Ser Ile Ala Thr Gly Val Phe Ala Glu Lys Val Tyr	
85 90 95	
gac ttt cat aag aac tac att gag tgt gct gaa aac tta tac aat gct	336
Asp Phe His Lys Asn Tyr Ile Glu Cys Ala Glu Asn Leu Tyr Asn Ala	
100 105 110	
aaa gtg gaa aga gtt gac ttc aca aat gat gta caa gat acc aga ttt	384
Lys Val Glu Arg Val Asp Phe Thr Asn Asp Val Gln Asp Thr Arg Phe	
115 120 125	
aaa att aat aaa tgg att gaa aat gag aca cat gga aag atc aag aag	432
Lys Ile Asn Lys Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys	
130 135 140	
gtg ttg ggc gac agc agc ctc agc tcg tcg gct gtc atg gtg ctg gtg	480
Val Leu Gly Asp Ser Ser Leu Ser Ser Ser Ala Val Met Val Leu Val	
145 150 155 160	
aac gct gtt tac ttc aaa ggc aaa tgg aaa tcg gcc ttc acc aag act	528
Asn Ala Val Tyr Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Thr	
165 170 175	
gat acc ctc agt tgc cgt ttt agg tct ccc acg tgt cct gga aaa gta	576
Asp Thr Leu Ser Cys Arg Phe Arg Ser Pro Thr Cys Pro Gly Lys Val	
180 185 190	
gtt aat atg atg cat caa gaa cgg cgg ttc aat ttg tct acc att cag	624
Val Asn Met Met His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln	
195 200 205	
cag cca cca atg cag gtt ctt gag ctc caa tat cat ggt ggc ata agc	672
Gln Pro Pro Met Gln Val Leu Glu Leu Gln Tyr His Gly Gly Ile Ser	
210 215 220	
atg tac att atg ctg cct gag gat ggc cta tgt gaa att gaa agc aag	720
Met Tyr Ile Met Leu Pro Glu Asp Gly Leu Cys Glu Ile Glu Ser Lys	
225 230 235 240	
ctg agt ttc cag aat ctg atg gac tgg acc aat agg agg aaa atg aaa	768
Leu Ser Phe Gln Asn Leu Met Asp Trp Thr Asn Arg Arg Lys Met Lys	
245 250 255	
tct cag tat gtg aac gtg ttt ctc ccc cag ttc aag ata gag aag aat	816
Ser Gln Tyr Val Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asn	
260 265 270	
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Tyr Glu Met Thr His His Leu Lys Ser Leu Gly Leu Lys Asp Ile Phe	
275 280 285	
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Asp Glu Ser Ser Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu	
290 295 300	

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 Tyr Val Ser Lys Leu Met His Lys Ser Phe Ile Glu Val Ser Glu Glu
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 Gly Thr Glu Ala Thr Ala Ala Thr Glu Asn Asn Ile Val Glu Lys Gln
 325 330 335
 ctt cct gag tcc aca gtg ttc aga gcc gac cgc ccc ttt ctg ttt gtc 1056
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 340 345 350
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 <213> Mus musculus

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 Gly Ala Arg Gly Asp Cys Ala Arg Gln Ile Asp Lys Ala Leu His Phe
 35 40 45
 Asn Ile Pro Ser Arg Gln Gly Asn Ser Ser Asn Asn Gln Pro Gly Leu
 50 55 60
 Gln Tyr Gln Leu Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys
 65 70 75 80
 Asp Tyr Glu Leu Ser Ile Ala Thr Gly Val Phe Ala Glu Lys Val Tyr
 85 90 95
 Asp Phe His Lys Asn Tyr Ile Glu Cys Ala Glu Asn Leu Tyr Asn Ala
 100 105 110
 Lys Val Glu Arg Val Asp Phe Thr Asn Asp Val Gln Asp Thr Arg Phe
 115 120 125
 Lys Ile Asn Lys Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys
 130 135 140
 Val Leu Gly Asp Ser Ser Leu Ser Ser Ser Ala Val Met Val Leu Val
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<210> 10
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<220>
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<210> 11
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<220>
<223> Description of Artificial Sequence:synthesis

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<210> 12
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<220>
<223> Description of Artificial Sequence:synthesis

<400> 12
aatggtggca taaacatg 18

<210> 13
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<220>
<223> Description of Artificial Sequence:synthesis

<400> 13
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<220>
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthesis

<400> 24
gtgaatgctg tgtacttaaa ggcaantgn 29

<210> 25
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthesis

<400> 25
aanagraang grtcngc 17

<210> 26
<211> 26
<212> DNA
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<220>
<223> Description of Artificial Sequence:synthesis

<400> 26
atggcntcng cngcngcngc naaygc 26

<210> 27
<211> 37
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<220>
<223> Description of Artificial Sequence:synthesis

<400> 27
cgacctccag aggcaattcc agagagatca gccctgg 37

<210> 28
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<220>
<223> Description of Artificial Sequence:synthesis

<400> 28
gtcttccaag cctacagatt tcaagtggct cctc

34

<210> 29
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<212> DNA
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<220>
<223> Description of Artificial Sequence:synthesis

<400> 29
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30

<210> 30
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<220>
<223> Description of Artificial Sequence:synthesis

<400> 30
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27

<210> 31
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<220>
<223> Description of Artificial Sequence:synthesis

<400> 31
gaggtctcag aagaaggcac tgaggcaact gctgcc

36

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<220>
<223> Description of Artificial Sequence:synthesis

<400> 32
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19

<210> 33
<211> 19
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<220>
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<400> 33
gaaacaaatc aaagcaaac

19

<210> 34
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<220>
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<400> 34
gaaattgaaa rcaarctgas yttycagaat

30

<210> 35
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthesis

<400> 35
ctgasyttyc agaattctaat ggamtggac

29

<210> 36
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<220>
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<400> 36
ggaytsaggr agtwgctttt cwacratrtt

30

<210> 37
<211> 36
<212> DNA
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<220>
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<400> 37
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36

<210> 38
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 38
ccagtgcaga tctctctgga attgcctctg gaggtcgtc 39

<210> 39
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
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<400> 39
gcctgttact gtataggaaa ccaaaccg 28

<210> 40
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<220>
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<400> 40
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<210> 41
<211> 24
<212> DNA
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<220>
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<400> 41
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<210> 42
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<220>
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<400> 42
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<210> 43
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
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<400> 43
atggatccgc cgccatggcc tcccttgctg cagcaaatgc agag

44

<210> 44
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthesis

<400> 44
tatactgagg cagtgttaac aagcaac

27